PROFILING TUMOR SPECIFIC MARKERS FOR THE DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE

Related Applications

[0001] This application claims priority to U.S. Provisional Patent Application No. 60/249,508, filed on November 16, 2000, which is hereby incorporated by reference in its entirety.

Field of the Invention

[0002] The description below relates to the use of marker systems found in a subject for the diagnosis of neoplastic diseases, including tumors with neural and neuroendocrine differentiation. In a preferred embodiment, a subject's auto-antibody profile is developed and molecular characteristics of a particular neoplasm afflicting the subject are determined.

Background of the Invention

[0003] The American Cancer Society predicts that 1.27 million new cases of cancer will be diagnosed in the United States in 2001. The number of cancer-related deaths for 2001 are predicted to include: 157,400 deaths from lung cancer, 31,500 deaths from prostate cancer, 40,000 deaths from breast cancer, and 56,700 deaths from colorectal cancer. Lung, prostate, breast, and colon cancer are the most common tumors.

[0004] Early detection of neoplastic disease (cancer) is critical to ensure favorable treatment of the disease. When patients go to seek for treatment, they are generally presenting with symptoms due to distant metastases, meaning that too often the cancer is detected too late. Therefore, the ability to detect and diagnose cancer through the identification of tumor markers is an area of widespread interest.

[0005] It is therefore of interest to identify early stage cancers with neural and/or neuroendocrine components/differentiation in a minimally invasive manner. In particular, it would be a great boon to the treatment of cancers to identify an array of tumor-associated antigens that are specific for the cancer type. An antibody raised against such antigens can be used in the diagnosis and targeted treatment of neoplastic diseases. Auto-antibodies against

such antigens generated as a part of subject's immune response can be used in the diagnosis of neoplastic diseases.

Summary of the Invention

[0006] The disclosure below encompasses a method for determining the presence of neoplastic molecular markers in a host comprising: a) obtaining a test sample from the host, wherein the host is suspected of having a neoplastic disease, b) determining the presence of one or more neoplastic molecular markers in the test sample, and c) analyzing the presence of one or more neoplastic molecular markers, wherein the analysis permits the identification of the neoplastic disease. Examples of neoplastic diseases that can be detected by the disclosed methods include lung cancer, prostate cancer, neuroblastoma and astrocytoma.

[0007] The disclosure further encompasses an array of neoplastic molecular markers arranged in an assayable format.

[0008] Further, the methods disclosed relate to a method of diagnosing a neoplastic disease comprising: providing an assay sample isolated from a subject suspected of having a neoplasm, determining the presence of one or more neoplastic molecular markers in the subject, and identifying the neoplastic disease from the presence of neoplastic molecular markers determined.

[0009] A method of treating a neoplastic disease is also disclosed. This method comprises providing an assay sample isolated from a subject suspected of having a neoplasm, determining the presence of one or more neoplastic molecular markers in the sample, identifying the neoplastic disease from the presence of neoplastic molecular markers determined, and selecting a therapeutic protocol based upon a correlation between particular therapeutic regimes and particular neoplastic disease states.

Detailed Description of the Preferred Embodiment

[0010] The description below relates to the molecular characterization of a variety of neoplastic diseases based on qualitative and quantitative characteristics of the particular neoplasm. The term "molecular characterization" relates to the use of various biochemical markers to identify the presence of a neoplasm in a subject and further to positively identify

the specific type of neoplasm afflicting the subject. In a preferred embodiment, changes in expression patterns of various genes associated with a neoplastic disease or in a subject's blood antibody profile are used as neoplastic molecular markers with which to identify neoplastic disease for therapeutic and diagnostic purposes.

[0011] Determining the presence of particular neoplastic molecular markers is achieved using a number of well-known techniques that indicate the presence of a particular set of markers. For example, immunological assays can be used to determine the presence of a subject's immunogenic response to a neoplastic molecular marker. Biochemical assays that determine gene expression levels and other indicia of increased expression in a cell can also be used with the methods described herein.

[0012] As used herein, an array of neoplastic molecular markers refers to a non-random arrangement of markers or reagents in a matrix for the detection of neoplastic markers. The array can be in any form that will permit the detection of the presence of particular neoplastic molecular markers. For example, the array can be assembled on a multi-well plate, in an assembly of tubes, or immobilized to a structure. In one embodiment, a typical multi-well plate can be used assay a matrix for an array of peptides against which the presence of particular antibodies is detected. In another embodiment, the multi-well plate contains various PCR primer pairs that are used to amplify a particular message. In another embodiment, probes can be immobilized to a matrix for detection, as is described in U.S. Patent No. 6,303,288, which is hereby incorporated by reference in its entirety.

<u>Neoplasms</u>

[0013] The spectrum of disease states commonly referred to as cancer all relate to various types of uncontrolled or neoplastic cell growth. As a normal cell transitions from a normal phenotype to a neoplastic phenotype, the gene expression patterns of the normal cell change from a normal phenotype expression pattern to a neoplastic phenotype expression pattern. Moreover, these neoplastic gene expression patterns are different, depending on the source and nature of the neoplasm.

[0014] Neoplastic phenotypes have a number of characteristics that can be exploited for diagnostic and therapeutic purposes. For example, a neoplastic cell can be characterized by the loss or acquisition of cell surface antigenic components as compared to a

wildtype cell. A neoplastic cell may also demonstrate the acquisition of neoantigen expression that is absent from a normal cell. Alternatively, a neoplastic cell can demonstrate an increase in the expression of various genes, particularly transcription factors, as compared to a normal cell. Additionally, a neoplastic cell can demonstrate changes that influence cell-cell interactions in the host. These are just a few examples of the numerable alterations in gene expression patterns typically present in a neoplastic cell. As disclosed below, the various genes that are differentially expressed in a neoplastic cell can be used as neoplastic molecular markers for diagnostic and therapeutic purposes.

Neoplastic Molecular Markers

[0015] Neoplastic molecular markers are biochemical markers arising from or related to genes that are differentially or differently expressed by neoplastic cells as compared to a normal or non-neoplastic cell. The normal function of the genes that constitute a neoplastic molecular marker is not significant to the disclosed methods. Accordingly, the function of such markers vary and include but are not limited to metabolic proteins, structural proteins, regulatory proteins, signaling proteins, secretory proteins, apoptotic proteins, mitochondrial proteins, glycoproteins, and glycolipids.

[0016] In some cases, neoplastic molecular markers are expressed in normal cells as well as by neoplastic or tumor cells. In tumor cells however, the expression of the neoplastic molecular marker gene is in some way atypical a compared to a normal cell. For example, the expression pattern of a neoplastic molecular marker gene may be greatly increased or greatly decreased when compared to the expression pattern of the marker gene in a non-neoplastic cell.

[0017] Another example of differential activity of a neoplastic molecular marker comprises post-translational modifications of the protein produced from the expressed marker gene. Alterations of the post-translational modifications made to the neoplastic molecular marker may alter the immunological characteristics of the protein, *e.g.*, may make the gene product immunogenic to the subject whereas the wildtype form of the protein is not immunogenic. Additionally various functional characteristics of the produced protein may be altered in the neoplastic state. Example of a functional characteristic that can be altered in a neoplastic cell as compared to a wildtype cell is the level of activity exhibited by an enzyme

or the half-life of a cell surface marker on the surface of the host cell. Further, a neoplastic molecular marker might may be released or shed from a neoplastic cell while the protein is retained in the normal cell. These are just a few examples of how a gene that is normally expressed in a non-neoplastic cell can be differentially expressed in a neoplastic cell.

Transcription Factors as Neoplastic Molecular Markers

[0018] Often in neoplasmic systems, distinct expression patterns of transcriptional modulators can be used to identify neoplasms in a subject. Accordingly, the molecular characterization of transcriptional modulator expression profiles can be used to identify the presence of particular neoplasms in a subject.

[0019] Transcriptional modulators include factors that alter chromatin structure to permit access of the transcriptional components to the target gene of interest. One group of promoter restructuring factors that perturbs chromatin in an ATP-dependent manner includes NURF, CHRAC, ACF, the SWI/SNF complex, and SWI/SNF-related (RUSH) proteins.

[0020] Another group of transcription modulating factors is involved in the recruitment of a TATA-binding protein (TBP)-containing and not-containing (Initiator) complexes. Examples of general initiation factors include: TFIIB, TFIID, TFIIE, TFIIF, and TFIIH. Each of these general initiation factors are thought to function in intimate association with RNA polymerase II and are required for selective binding of polymerase to its promoters. Additional factors such as TATA-binding protein (TBP), TBP-homologs (TRP, TRF2), initiators that coordinate the interaction of these proteins by recognizing the core promoter element TATA-box or initiator sequence and supplying a scaffolding upon which the rest of the transcriptional machinery can assemble are also considered transcription modulating factors.

[0021] Further, TBP-associated factors (TAFs) that function as promoter-recognition factors, as coactivators capable of transducing signals from enhancer-bound activators to the basal machinery, and even as enzymatic modifiers of other proteins are also transcription modulators. Particular examples of transcription modulators include: the TAFIIA complex: (TAFIIAa; TAFIIAb; TAFIIAg); the TAFIIB complex: (TAFIIB; RAP74; RAP30); TAFs forming the TFIID complex (TAFII250; CIF150; TAFII130/135; TAFII100; TAFII70/80; TAFII31/32; TAFII20; TAFII15; TAFII28; TAFII68; TAFII55; TAFII30;

TAFII18; TAFII105); the TAFIIE complex: (TAFIIEa; TAFIIEb); the TAFIIF complex (p62; p52; MAT1; p34; XPD/ERCC2; p44; XPB/ERCC3; Cdk7; CyclinH); the RNA polymerase II complex: (hRPB1, hRPB2, hRPB3, hRPB4, hRPB5, hRPB6, hRPB7, hRPB8, hRPB9, hRPB10, hRPB11, hRPB12); and others.

[0022] Mediators that act as a conserved interface between gene-specific regulatory proteins and the general transcription apparatus of eukaryotes are also considered to be transcription modulators. Typically, this type of mediator complex integrates and transduces positive and negative regulatory information from enhancers and operators to promoters. They typically function directly through RNA polymerase II, modulating its activity in promoter-dependent transcription. Examples of such mediators that form coactivator complexes with TRAP, DRIP, ARC, CRSP, Med, SMCC, NAT, include: TRAP240/DRIP250; TRAP230/DRIP240; DRIP205/ CRSP200/TRIP2/PBP/RB18A/TRAP220; hRGR1/CRSP150/DRIP150/TRAP170, TRAP150; CRSP130/hSur-2/DRIP130; TIG-1; CRSP100/TRAP100/DRIP100; DRIP97; DRIP92/TRAP95; CRSP85; CRSP77/DRIP77/TRAP80; CRSP70/DRIP70; Ring3; hSRB10/hCDK8; DRIP36/hMEDp34; CRSP34; CRSP33/hMED7; hMED6; hSRB11/hCyclin C; hSOH1; hSRB7; and others. Additional modulators in this class include proteins of the androgen receptor complex, such as: ANPK; ARIP3; PIAS family (PIASα, PIASβ, PIASγ); ARIP4; and transcriptional co-repressors such as: the N-CoR and SMRT families (NCOR2/SMRT/TRAC1/CTG26/TNRC14/ SMRTE); REA; MSin3; HDAC family (HDAC5); and other modulators such as: PC4; MBF1.

[0023] Another class of transcription modulators comprises enhancer-bound activators and sequence-specific or general repressors. Examples of these modulators include: non-tissue specific bHLHs, such as: USF; AP4; E-proteins (E2A/E12, E47; HEB/ME1; HEB2/ME2/MITF-2A,B,C/SEF-2/TFE/TF4/R8f); TFE family (TFE3, TFEB); the Myc, Max, Mad families; WBSCR14; and others.

[0024] Another example of this class of transcriptional modulators is the neuronally enriched bHLHs such as: Neurogenins (Neurogenin-1/MATH4c, Neurogenin-2/MATH4a, Neurogenin-3/MATH4b); NeuroD (NeuroD-1, NeuroD-2, NeuroD-3(6)/ my051/NEX1/MATH2/Dlx-3, NeuroD-4/ATH-3/ NeuroM); ATHs (ATH-1/MATH1, ATH-5/MATH5); ASHs (ASH-1/MASH1, ASH-2/MASH2, ASCL-3/reserved); NSCLs (NSCL1/HEN1,

NSCL2/HEN2), HANDs (Hand1/eHAND/Thing-1, Hand2/dHAND/Thing-2); Mesencephalon-Olfactory Neuronal bHLHs: COE proteins (COE1; COE2/Olf-1/EBF-LIKE3, COE3/Olf-1 Homol/Mmot1); and others.

[0025] Other examples of this class of transcriptional modulators includes: the Glia enriched bHLHs, such as: OLIG proteins (Olig1, Olig2/protein kinase C-binding protein RACK17, Olig3), and others; the bHLH family of negative regulators, which include: Ids (Id1, Id2, Id3, Id4), DIP1, HES (HES1, HES2, HES3, HES4, HES5, HES6, HES7, SHARPs (SHARP1/DEC-2/eip1/Stra13, SHARP2/DEC-1/TR00067497_p), Hey/HRT proteins (Hey1/HRT1/HERP-2/HESR-2, Hey2/HRT2/HERP-1, HRT3), and others. There are other bHLHs that fall within this present category of transcription modulators, which include: Lyl family (Lyl-1, Lyl-2); RGS family (RGS1, RGSRGS2/G0S8, RGS3/RGP3); capsulin; CENP-B; Mist1; Nhlh1; MOP3; Scleraxis; TCF15; bA305P22.3; Ipf-1/Pdx-1/Idx-1/Stf-1/Iuf-1/Gsf; and others.

[0026] Transcription factors belonging to Wnt pathway are also transcription modulators of the present class. Examples of such proteins include: β-catenin; GSK3; Groucho proteins (Groucho-1, Groucho-2, Groucho-3, Groucho-3); TCF family (TCF1A, B, C, D, E, F, G/ LEF-1; TCF3; TCF4) and others.

[0027] Transcription factors belonging to Notch pathway are also transcription modulators of the present class. Examples of such proteins include: Delta, Serrate, and Jagged families (Dll1, Dll3, Dll4, Jagged1, Jagged2, Serrate2); Notch family (Notch1, Notch2, Notch3, Notch4, TAN-1); Bearded family (E(spl)mα, E(spl)m2, E(spl)m4, E(spl)m6); Fringe family (Mfng, Rfng, Lfng); Deltex/dx-1; MAML1; RBP-Jk/CBF1/Su(H)/KBF2; RUNX; and others.

[0028] Transcription factors belonging to TGFβ/BMP pathway are also transcription modulators of the present class. Examples of such proteins include: Chordin; Noggin; Follistatin; SMAD proteins (SMAD1, SMAD2, SMAD3, SMAD4, SAMD5, SMAD6, SMAD7, SMAD8, SMAD9, SMAD10); and others.

[0029] Transcription factors belonging to Sonic hedgehog pathway are also transcription modulators of the present class. Examples of such proteins include: SHH; IHH; Su(fu); GLI family (GLI/GLI1, Gli2, Gli3); Zic family (Zic/Zic1, Zic2, Zic3); and others.

[0030] Wing helix/ forkhead family of transcription factors are also transcription modulators of the present class. Examples of such proteins include: BF proteins (BF1, BF2); and others.

[0031] HMG transcription factors are also transcription modulators of the present class. Examples of such proteins include: Sox proteins (Sox1, Sox2, Sox3, Sox4, Sox6, Sox10, Sox11, Sox13, Sox14 Sox18, Sox21, Sox22, Sox30); HMGIX; HMGIC; HMGIY; HMG-17; and others.

[0032] Homeodomain transcription factors pathway are also transcription modulators of the present class. Examples of such proteins include: Hox proteins; Evx family (Evx1, Evx2); Mox family (Mox1, Mox2); NKL family (NK1, NK3, Nkx3.1, NK4); Lbx family (Lbx1, Lbx2); Tlx family (Tlx1, Tlx2, Tlx3); Emx/Ems family (Emx1, Emx2); Vax family (Vax1, Vax2); Hmx family (Hmx1, Hmx2, Hmx3); NK6 family (Nkx6.1); Msx/Msh family (Msx-1, Msx-2); Cdx (Cdx1, Cdx2); Xlox family (Lox3); Gsx family (Goosecoid, GSX, GSCL); En family (En-1, En-2) HB9 family (Hb9/HLXB9); Gbx family (Gbx1,Gbx2), Dbx family (Dbx-1, Dbx-2); Dll family (Dlx-1, Dlx-2, Dlx-4, Dlx-5, Dlx-7); Iroquois family (Xiro1, Irx2, Irx3, Irx4, Irx5, Irx6); Nkx (Nkx2.1/TTF-1, Nkx2.2/TTF-2, Nkx2.8, Nkx2.9, Nkx5.1, Nkx5.2); PBC family (Pbx1a, Pbx1b, Pbx2, Pbx3); Prd family (Otx-1, Otx-2, Phox2a, Phox2B); Ptx family (Pitx2, Pitx3/Ptx3), XANF family (Hesx1/XANF-1); BarH family (BarH, Brx2); Cut; Gtx; and others.

[0033] POU domain factors are also transcription modulators of the present class. Examples of such proteins include: Brn2/XlPou2; Brn3a, Brn3b; Brn4/POU3F4; Brn5/Pou6F1; and others.

[0034] Transcription factors with homeodomain and LIM regions are also transcription modulators of the present class. Examples of such proteins include: Isl1; Lhx2; Lhx3; Lhx4; Lhx5; Lhx6; Lhx7 Lhx9; LMO family (LMO1, LMO2, LMO4); and others.

[0035] Paired box transcription factors are also transcription modulators of the present class. Examples of such proteins include: Pax2; Pax3; Pax5; Pax6; Pax7; Pax8; and others.

[0036] Fork head/winged helix transcription factors are also transcription modulators of the present class. Examples of such proteins include: BF-1; BF-2/Freac4; Fkh5/Foxb1/HFH-e5.1/Mf3; Fkh6/Freac7; and others.

[0037] Zinc finger transcription factors are also transcription modulators of the present class. Examples of such proteins include: GATA family (Gata1, Gata2, Gata3, Gata4/5, Gata6); MyT family (MyT1, MyT1l, MyT2, MyT3); SAL family (HSal1, Sal2, Sall3); REST/NRSF/XBR; Snail family (Scratch/Scrt); Zf289; FLJ22251; MOZ; ZFP-38/RU49; Pzf; Mtsh1/teashirt; MTG8/CBF1A-homolog; TIS11D/BRF2/ERF2; TTF-I interacting peptide 21; Znf-HX; Zhx1; KOX1/NGO-St-66; ZFP-15/ZN-15; ZnF20; ZFP200; ZNF/282; HUB1; Finb/RREB1; Nuclear Receptors (liganded: ER family; TR family; RAR familiy; RXR family; PML-RAR family; PML-RXR family; orphan receptors: Not1/Nurr; ROR; COUP-TF family (COUP-TF1, COUP-TF2)) and others.

[0038] RING finger transcription factors are also transcription modulators of the present class. Examples of such proteins include: KIAA0708; Bfp/ZNF179; BRAP2; KIAA0675; LUN; NSPc1; Neuralized family (neu/Neur-1, Neur-2, Neur-3, Neur-4); RING1A; SSA1/RO52; ZNF173; PIAS family (PIAS-α, PIAS-β, PIAS-γ, PIAS-γ homolog); parkin family; ZNF127 family and others.

[0039] Another class of transcription modulators includes proteins relating to cell-cycle progression-dedicated components that are part of the RNA polymerase II transcription complex. Examples of these proteins include: E2F family (E2F-1, E2F-3, E2F-4, E2F-5); DP family (DP-1, DP-2); p53 family (p53, p63; p73); mdm2; ATM; RB family (RB, p107, p130).

[0040] Still another class of transcription modulators includes proteins relating to capping, splicing, and polyadenylation factors that are also a part of the RNA polymerase II modulating activity. Factors involved in splicing include: Hu family (HuA, HuB, HuC, HuD); Musashi1; Nova family (Nova1, Nova2); SR proteins (B1C8, B4A11, ASF SRp20, SRp30, SRp40, SRp55, SRp75, SRm160, SRm300); CC1.3/CC1.4; Def-3/RBM6; SIAHBP/ PUF60; Sip1; C1QBP/GC1Q-R/HABP1/P32; Staufen; TRIP; Zfr; and others. Polyadenylation factors include: CPSF; Inducible poly(A)-Binding Protein (U33818), and others.

[0041] Each of the factors discussed above is controlled by positive and negative regulatory mechanisms to achieve coordinated expression of genes associated with the same physiological process (differentiation, for example.) Uncontrollable proliferation of dedifferentiated mature cells or stem and progenitor cells leads to tumor development because many elements in the network of cellular transcriptional modulators that should be coordinately controlled are missing (not expressed or not expressed at sufficient quantities), or are inactive (additional complex components not available or improperly expressed). Given that the activity and developmental potential of every cell is characterized by the network of transcription modulatory factors, cells have only a limited capacity to respond to certain external stimuli and treatment protocols. Each of these systems can be used to characterize and identify neoplasms.

Immunological and Molecular Characterization of Subject's Response to Neoplasm

[0042] A variety of assay systems can be used to characterize and identify the presence and type of neoplastic cells in a subject. These techniques have utility in neoplasm characterization as they target particular molecular components of the tumor cell or by examining changes in a subject in response to the presence of a neoplasm. For example, well-known immunological assays can be used to identify the presence of antigenic markers that indicate the presence of a neoplasm. Similarly, molecular biology-based assays can be used to measure and compare the expression levels of particular genes that have expression patterns identified as differing between normal and neoplastic cells.

Immunological Characterization

[0043] The immunogenic properties of neoplastic molecular markers can be exploited to identify a neoplastic disease. Components of the immune response elicited from a host with a neoplasm can be used to characterize the nature of that neoplasm or the neoplastic cell. Phenotypic changes in neoplastic cell's gene expression patterns can elicit a measurable immune response from the host organism harboring the neoplastic cell. This immune response can be used to more accurately identify and characterize a neoplasm, which in turn is used to define the most effective strategy for the treatment of the neoplasm.

[0044] Immune responses are generally classified as being cellular or humoral in nature. A cellular immune response is characterized by the activation and deployment of

various immune system cell types such as NK cells, T cells, lymphocytes, macrophages, and the like. A humoral immune response relates to small molecules such as cytokines, complement proteins, antibodies, and the like. Quantifiable elements of both the cellular and humoral immune responses can be exploited to characterize neoplasms.

[0045] Any sample source from a subject can be used to analyze an immune response of a host to a neoplastic disease. Examples of sample sources include blood, tears, semen, saliva, urine, or other bodily fluids.

[0046] Detection of neoplastic molecular markers present in a subject is currently used as a diagnostic for the presence of a malignancy or neoplasm in the body of a host. For example, the immunological detection of dopamine derivatives in the urine is presently used as a diagnostic for neoplasmic afflictions such as pheochromocytoma or neuroblastoma.

[0047] Using various immunological assay techniques, most human tumors have been reported to have new antigens that are foreign to the host and correlated to the neoplasm. For example, human tumors that have been shown to be antigenic include melanoma, neuroblastoma, astrocytoma, uroepithelial carcinoma, ovarian carcinoma, sarcoma, and colon carcinoma.

[0048] Existing assays are valuable but often limited diagnostic tools. One limitation of the existing technology arises from the fact that the markers used in these assays are often too general and not tumor specific. Because they lack specificity, current neoplastic markers do not provide the means by which a diagnostician can identify and characterize the presence of a neoplasm with precision.

[0049] The methods provided herein allow for the identification and characterization of neoplastic cells by exploiting tumor associated antigens (TAAs), their gene and protein expression patterns as well as tumor associated antibodies (TABs). Differentiating between normal and neoplastic cells using a TAA target is possible by exploiting qualitative and quantitative differences in gene expression of the target marker between the two cell types. Differentiating between normal and subjects with neoplastic disease using a TAB target is possible by exploiting qualitative and quantitative differences in the auto-immune response (presense of auto-antibodies against/specific to or recognizing the target marker protein) between the two blood samples.

[0050] It will be appreciated that TAAs and TABs can literally mean antigens or auto-antibodies, respectively, specific to a particular tumor or neoplastic disease. Alternatively, TAAs can refer to an altered expression pattern of a normal cell protein in a neoplastic cell. Alternatively, TABs can refer to an altered immune-response of a normal host compared with a subject with a neoplastic disease.

Transcription Factor-Derived Peptides For Identification of TABs

[0051] A tumor-associated antibody (TAB) profile of a patient with a tumor or neoplasm can be used to determine the molecular subtype of the tumor. The term "TAB" is used throughout the specification to refer to an immune response generated by a host in response to a tumor or neoplasm. This term encompasses other modalities of an immune response, such as the generation of cellular components with specificity to the TAB of a subject's tumor.

[0052] A subject's TAB profile is assembled by identifying tumor specific antibodies or other immune system components that are produced by the subject in response to the presence of a tumor. In a preferred embodiment, antibodies that a subject generates against a tumor are used to produce a TAB profile.

[0053] Screening for host antibodies (TABs) that bind to specific tumor markers or TAAs can be performed using any of a variety of well-known immunological techniques. For example, peptides or full-length proteins of potential TAAs can be bound to microtiter plates or membranes (dot or slot blot). For example, enzyme-linked immunoadsorbant assay (ELISA) can be used to determine the TAB profile of a patient.

[0054] Using a standard ELISA protocol, microtiter plates are incubated with a patients' serum samples followed by several washes. To identify human TABs that have bound to peptides or proteins, the microtiter plates are incubated with antihuman Ig antibodies conjugated to a reporter such as alkaline phosphatase or peroxidase. It will be appreciated that the antihuman antibodies are be conjugated to a radioisotope or fluorescent day to provide visualization of binding. The presence of human antibodies is visualized using color reaction for alkaline phosphatase or peroxidase.

[0055] Suitable peptides corresponding to transcriptional regulators employed to identify tumor specific or tumor enriched antibodies in a patient's blood are detailed in Tables 1-8.

Table 1

Helix-loop-helix transcription factors

Neurogenin family	
Neurogenin 1	QDDEQERRRRRGRTR (SEQ ID NO: 1)
Neurogenin 2	CKRRPSRSRAVSR (SEQ ID NO:2)
Neurogenin 3	QRRSRRKKANDRER (SEQ ID NO:3)
NeuroD family	
NeuroD 1	DDDQKPKRRGPKKKKM (SEQ ID NO:4)
NeuroD 2	QDSSPDHEKSYH (SEQ ID NO:5)
NeuroD 3	GTLDNSKSMKP (SEQ ID NO:6)
ATH family	
ATH1	SFNNDKKLSKYET (SEQ ID NO:7)
ATH5	GLRCEQRGRDHPY (SEQ ID NO:8)
ASH family	
ASH-1	ADGQPSGGGHKSA (SEQ ID NO:9)
NSCL family	
NSCL 1	PTHSETESGFSDCGGGA (SEQ ID NO:10)
NSCL 2	AADSDHPSSAHSDPES (SEQ ID NO:11)
HES	
HES 1	TPDKPKTASEH (SEQ ID NO:12)
HES 2	SLKPLLEKRRRAR (SEQ ID NO:13)
HES 3	RREGSTTDSANP (SEQ ID NO:14)
HES 5	SLHQDYSEGYSWC (SEQ ID NO:15)
SHARP-family	
SHARP 1	CKPKRSLKRDDTKDT (SEQ ID NO:16)
SHARP 2	VYKSRRGIKRSEDSKE (SEQ ID NO:17)
Hey /HRT-family	
Hey 1	TASPTEPHHQGRLG (SEQ ID NO:18)

Hey 2	SPQQTSSGTNNKPYRPW (SEQ ID NO:19)
Hey L	STPSSSQMQARKKR (SEQ ID NO:20)

Table 2

Homeodomain transcription factors

BarH family	
BarH2	TWYQNRRTKWKR (SEQ ID NO:21)
Bcd family	
Ptx3/PITX3	FKNRRAKWRKRERSQ (SEQ ID NO:22)
Dll family	
Dlx1	AGHSQPDGAYSSA (SEQ ID NO:23)
Dlx2	HQHQQPPSGGGAGPGG (SEQ ID NO:24)
Dlx5	HPSQESPTLPESSATDS (SEQ ID NO:25)
Ems family	
Emx-2	GSDSQQKKKGTHH (SEQ ID NO:26)
En family	
En-1	PRTRKLKKKKNEK (SEQ ID NO:27)
En-2	APGNHQHPHRITNF (SEQ ID NO:28)
Gbx family	
Gbx2	STRRRQRPASSRRSRC (SEQ ID NO:29)
Iroquois (Irx) family	
Irx2a	GGNEGSPCPPCPG (SEQ ID NO:30)
NK-2 family	
Nkx-2.2	PPQDSSSKSPEPS (SEQ ID NO:31)
Nkx-2.9	QDAKPRVRREQQTCV (SEQ ID NO:32)
Nkx-5.1	DERPAHKDGPTEAS (SEQ ID NO:33)
Nkx-5.2	PHGPKEPSPKHHT (SEQ ID NO:34)
Prd family	
Phox2a	CSSEDDDSKESTCSPT (SEQ ID NO:35)

Phox2b	GSSGKKSDSSRDDES (SEQ ID NO:36)

Table 3

POU domain transcription factors

Brn-5 family	
Brn-5	KPSTPESPAKSE (SEQ ID NO:37)

Table 4

LIM region containing transcription factors

Isl-1	LRPHVHKQPEKTTR (SEQ ID NO:38)
Lhx2	RDQPYPSSQKTKRMRT (SEQ ID NO:39)
Lhx3	CFSRGESVYCKDDFF (SEQ ID NO:40)
Lhx4	EDYETAKQNDDSEAGAK (SEQ ID NO:41)
Lhx5	PLQDDPKETDNSTSSDK (SEQ ID NO:42)
LMO4	CSTCRNRLVPGDR (SEQ ID NO:43)

Table 5

Fork head/winged helix transcription factors

BF-2	DNGSFLRRRKRFKRQ (SEQ ID NO:44)

Table 6

High mobility group transcription factors

Sox-family	
Sox-1	SEPSGSPPAPAHSRA (SEQ ID NO:45)
Sox-2	GNQKNSPDRVKR (SEQ ID NO:46)
Sox-3	QPPSMSSPPPPPA (SEQ ID NO:47)
Sox-10	KKDHPDYKYQPRRRKNG (SEQ ID NO:48)
Sox-11	DYPDYKYRPRKKPK (SEQ ID NO:49)

Table 7

Zinc finger transcription factors

Cys4 zinc finger of nuclear receptor type-family	
NOT1	ASQSYSYHSSGEYS (SEQ ID NO:50)
Cys2His2 zinc finger domain-family	
SALL1	DGDTEKGQPSRPTKSKD (SEQ ID NO:51)
SAL2	PDSLDQPQPMEQGS (SEQ ID NO:52)
SALL3	GYADSPSATPASRSPQR (SEQ ID NO:53)
Zic1	SPSTDNPTTSSLSP (SEQ ID NO:54)
Zic3	NSKDTTKTPSA (SEQ ID NO:55)

Table 8

Not-assigned transcription factors

RBP-Jk	KPSQKKQSLKNTD (SEQ ID NO:56)
TLE1/Groucho 1	DDKKHHDAEHHRDREPGT (SEQ ID NO:57)
TLE2/Groucho 2	KEPSGPYESDEDKSDY (SEQ ID NO:58)
TLE3/Groucho 3	STPSSKTKDLGHNDKSS (SEQ ID NO:59)
TLE4/Groucho 4	DYSSESKKQKTEEK (SEQ ID NO:60)

Molecular Biology Methods-Based Characterization of Neoplasms Molecular Characterization of Subject's Response to Neoplasm

[0056] In addition to the immunological methods discussed above, neoplasms can be characterized using molecular biology-based tools directed toward monitoring transcription factors and other TAAs expression patterns. Standard molecular biological techniques are employed for such characterization. For guidance regarding such techniques see, for example, Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Springs Harbor Press, N.Y.; and Ausubel et al., 1989, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. Examples of suitable assays include: Northern blot analysis, Southern blot analysis, Western blot analysis, RT-

PCR, PCR, nucleic acid sequence based amplification assays (NASBA), and transcription mediated amplification (TMA).

[0057] As with the immunological methods discussed above, any sample source from a subject can be used to analyze molecular changes in a subject in response to the presence of a neoplasm. Examples of sample sources include neoplastic cells in blood, tears, semen, saliva, urine, or other bodily fluids.

[0058] Detection of neoplastic molecular markers present in a subject is currently used as a diagnostic for the presence of a malignancy or neoplasm in the body of a host. For example, detection of cells with neoplastic molecular markers in the urine (using single-cell PCR method) is presently used as a diagnostic for neoplasmic afflictions such as prostate carcinoma. Cell surface marker and transcription factor expression patterns are two preferred targets for molecular identification and characterization.

[0059] A list of primer sequences that can be used to probe samples for the presence of particular neoplastic markers is provided below.

Table 9

Primer Sequences

Gene Name	GenBank ID	Oligo name	5' - 3'
Ash-1	L08424	N s II 24	gagcgcagccttagtaggagagga (SEQ ID NO:61)
	U77616	s 24	ccctctctgttcctgcacccaagt (SEQ ID NO:62)
		E s 28	ccagcATGgaaagctctgccaagatgg (SEQ ID NO:63)
		N as II 25	gacttgcttgggcgctgacttgtga (SEQ ID NO:64)
		N int as 26	gagcgcagtgtctccaccttactcat (SEQ ID NO:65)
		as 26 (Stop)	ccagttggtgaagtcgagaagctcct (SEQ ID NO:66)
Ath-1	U61148	s N 25	ctccattggctgagaagacacgcga (SEQ ID NO:67)
		s 26	gcgtccgagcctttgcagtgcaATGt (SEQ ID NO:68)
		as 25 (Stop)	ctccttcCTAacttgcctcatccga (SEQ ID NO:69)
		N int as 24	gtagcagctcggacaaggcgttga (SEQ ID NO:70)
Ath-5		s E 28	ccaccatgaagtcggcctgcaaacccca (SEQ ID NO:71)
		as E 24	catggggaagggctccggctggaa (SEQ ID NO:72)
BarH		s E 27	ccaccatgtagaaatgacagcaatgga (SEQ ID NO:73)
		as II E 23	gatggggttggacaaagggttga (SEQ ID NO:74)
BarH-2		s 24	catgatcgacgagatcctctccaa (SEQ ID NO:75)
		int as 25	ggttccgaagagggtattggcaact (SEQ ID NO:76)
BF-2		s E 27	gcgctatgaccctgagcacggagatgt (SEQ ID NO:77)
		as E 25	ggcgcgctaacgacgttcctaacaa (SEQ ID NO:78)

BMP-2	M22489	s 24 as 26	cggtccttgcgccaggtcctttga (SEQ ID NO:79) gtactagcgacacccacaaccctcca (SEQ ID NO:80)
BMP-6	M60315	s 24 as 25 (Stop)	cgacgcggacatggtcatgagctt (SEQ ID NO:81) ccccagcatctggtttcgagTTAgt (SEQ ID NO:82)
Brain-2		s 24 as 24	cgagagtcatggcgaccgcagcgt (SEQ ID NO:83) ccgtgaagctgggctgcgagtaga (SEQ ID NO:84)
Brain- 4/ XiPOU2	X82324	s 23 Int as 25 as 22 (Stop)	accATGgccacagctgcctcgaa (SEQ ID NO:85) cggagtgatcctggcaatggtgcga (SEQ ID NO:86) cctcgcttcctccagtcagaga (SEQ ID NO:87)
Brain- 5/ Pou6F1	NM_002702	s 24 (ATG) as 24	cattaccagcgccattcccagcAT (SEQ ID NO:88) cggtcgtagttgagctccttagca (SEQ ID NO:89)
Cdx-4	AF003530	s 25 as 26	gagcgtgtatcctgggccgtctagt (SEQ ID NO:90) cagagtcactttgcsccgagcctcca (SEQ ID NO:91)
Chordin	AF076612	s 24 as 24	gaccttcagtgccatcctgactct (SEQ ID NO:92) gtgcaggtgacagtgggtatccaa (SEQ ID NO:93)
Cux-2	AB006631	s 24 as 24	ggcagcatccaaggcagatgaagt (SEQ ID NO:94) ctccttgcccttcaccgtgagctt (SEQ ID NO:95)
Dlx-1		s E 28 as E 24	ggagatgaccatgaccaccatgccaga (SEQ ID NO:96) cacatcagttgaggctgctgcata (SEQ ID NO:97)
Dlx-2	U51003	s 26 as 27	gtggctgatatgcactcgacccagat (SEQ ID NO:98) cttggaccggcggttctggaaccagat (SEQ ID NO:99)
Dlx-5		s E 31 as E 23	ccgccatgacaggagtgtttgacagaagggt (SEQ ID NO:100) ctaatagagtgtcccggaggcca (SEQ ID NO:101)
Dlx-7	AF028235	s 26 as 25	cagcacctaaaccagcgtttccagca (SEQ ID NO:102) catcatctgaggcgaagccaggaca (SEQ ID NO:103)
Emx-1	AA775410 (5') X68879 (3')	s 24 as 24	cgtgttccccgaggccatgaacca (SEQ ID NO:104) gatgtcctccccattggcctgctt (SEQ ID NO:105)
Emx-2	X68880	s 25 as 28	cacaccccctattcgcctcgcagca (SEQ ID NO:106) ctatttcctccggactcgcctgcttggt (SEQ ID NO:107)
En-1		s E 25 as E 25	cgagcatggaagaacagcagccgga (SEQ ID NO:108) ggctactcgctctcgtctttgtcct (SEQ ID NO:109)
En-2		s E 25 as E 24	ccagcatggaggagaatgaccccaa (SEQ ID NO:110) cctactcgctgtccgacttgccct (SEQ ID NO:111)
GATA-1	X17254	N s 24 s 25 (ATG)	gggatcacactgagcttgccacat (SEQ ID NO:112) cccaggttaatccccagaggctccA (SEQ ID NO:113)

		as 26 (Stop)	CAtgagctgagcggagccaccacagt (SEQ ID NO:114)
GATA-2	M68891	s 24	caatcacctcgactcgcagggcaa (SEQ ID NO:115)
		as 26	gaggccacaggcattgcacaggtagt (SEQ ID NO:116)
GATA-3		s 24	gagcacagccgaggccatggaggt (SEQ ID NO:117)
		as 24	ccttgggcctggacttgcatccga (SEQ ID NO:118)
Gbx-2	U31468	s E 26 (ATG)	ctggcctctaccgagcgcgtctATGa (SEQ ID NO:129)
	NM_001485	s 25	ggagtagcaccgccttcagcataga (SEQ ID NO:120)
		as 24	gattgtcatccgagctgtagtcca (SEQ ID NO:121)
		as E 23 (Stop)	gccctggcccttctggacccTCA (SEQ ID NO:122)
Geminin	AF067855	s 23 (ATG)	ccatctacataATGaatcccagt (SEQ ID NO:123)
		as 22 (Stop)	gtggaggtaaacttcggcagta (SEQ ID NO:124)
GLI-1	X07384	s 24	gaccaagaagcgggcactgtccat (SEQ ID NO:125)
		as 26	gcgtgagtatgacttccggcacccctt (SEQ ID NO:126)
GLI-2	AB007298	s 25	ctcacctccatcaatgccacgccca (SEQ ID NO:127)
		as 24	ccaccagcatgtactgcgccttga (SEQ ID NO:128)
GLI-3	M57609	s 25	gcagctcttcagcaagtggctccta (SEQ ID NO:129)
		as 24	ctctcttgagcagtccagccacct (SEQ ID NO:130)
Glu Synthetase		s 28	ccaccatgaccacctcagcaagttccca (SEQ ID NO:131)
		as 24	cgatgtccctgccataggctctgt (SEQ ID NO:132)
Groucho-1/ TLE1	M99435	s E 24	ccgaaatgcagaggcactatgtga (SEQ ID NO:133)
		as E 24	cggagaagaagggtcctcattaga (SEQ ID NO:134)
Groucho-2		s E 25	gcaggatgtacccccagggaaggca (SEQ ID NO:135)
		as E 25	cctcagggcgacgctgtccgtggaa (SEQ ID NO:136)
Groucho-3/ TLE3		s E 23	ccaccatgtatccgcagggcaga (SEQ ID NO:137)
		as E 24	cgctcatctggggtgggatgttgt (SEQ ID NO:138)
Groucho-4		s E 24	cagagatgcagcggcattatgtca (SEQ ID NO:139)
		as E 25	gtactgccattggggtccttaggct (SEQ ID NO:140)
Hes-1	L19314	s E 25 (ATG)	ggaaaATGccagctgatataatgga (SEQ ID NO:141)
		s 24	ctaccccagccagtgtcaacacga (SEQ ID NO:142)
		as 26 (Stop)	gttccgccacggcctccacatggagt (SEQ ID NO:143)
Hes-2	4914512	s E 34	ccaccatgaagagcctgaagccgctgctggagaa (SEQ ID NO:144)
		s 24	gagcctgaagccgctgctggagaa (SEQ ID NO:145)
		as 24	ccgctctccgccacaggtgctcca (SEQ ID NO:146)
Hes-3		s E 24	gcccaccgatctccaagcctctga (SEQ ID NO:147)
		as E 24	ctacgtctcaccacggtcgccaca (SEQ ID NO:148)

Hes-5			s 26 as 26	gtggagatgctcagtcccaaggagaa (SEQ ID NO:149) ccgctggaagtggtaaagcagcttca (SEQ ID NO:150)
Hey-1/ HERP2	HRT1/	NM_012258	s E 30 (ATG) s 24 as 24 as E 25 (Stop)	ccagcATGaagcgagctcaccccgagtaca (SEQ ID NO:151) ggacagcgagctggacgagaccat (SEQ ID NO:152) ggctcagtgcattgggagacagta (SEQ ID NO:153) ccctccctcattctacatcagttct (SEQ ID NO:154)
Hey-2/ HERP1	HRT2/	NM_012259	s E 26 (ATG) s 24 as 25 as E 25	gacctccgagagcgacATGgacgaga (SEQ ID NO:155) ggctactttgacgcacacgctctt (SEQ ID NO:156) cactgctggtctgctgaggactgga (SEQ ID NO:157) ccaacttctgtcccccagggtcggt (SEQ ID NO:158)
HeyL			s 23 as 25	catgaagcgacccaaggagccga (SEQ ID NO:159) cagctcagaaagccccgatttcagt (SEQ ID NO:160)
Id-3			s 23 int as 23	cggctgctacgaggcggtgtgct (SEQ ID NO:161) ggagtgagctcggctgtctggat (SEQ ID NO:162)
Irx-2a		U90304	N s 26 (ATG) int as 24 as 23 (Stop)	accggtcgttccgATGgcagtggaga (SEQ ID NO:163) cgtcgttcttctccaggtcaatgt (SEQ ID NO:164) cgcgTTAaatgtcggacatacct (SEQ ID NO:165)
Irx-3		U90305 (5') AI217994 (3')	s 25 (ATG) as 25 (Stop)	cagccaccatgtccttcccacactt (SEQ ID NO:166) gaaCTAggatgaggagagagccgat (SEQ ID NO:167)
Lhx-2			s E 24 as E 24	ccgagatggaccgcagggccaaga (SEQ ID NO:168) gtggggtgaggggttgcgagtcat (SEQ ID NO:169)
Lhx-3			s E 25 as E 27	gaaccatggaggcgcgcggggagct (SEQ ID NO:170) gtcagaactgagcgtggtctacctcat (SEQ ID NO:171)
Lhx-4			s E 28 as E 26	gacgatgcaacagattccccagtgtgct (SEQ ID NO:172) gaggatggtccatctcatcgagccaa (SEQ ID NO:173)
Lhx-5			s E 26 as E 24	ggctatgatggtgcactgtgctggct (SEQ ID NO:174) cttaccatacggccgcttcgttga (SEQ ID NO:175)
LMO-4			s 27 as 24	catggtgaatccgggcagcagctcgca (SEQ ID NO:176) ccttctggtctggcagtagtggat (SEQ ID NO:177)
Med-6		AF074723	s 24 (ATG) as 25 (Stop)	gggaacctgtaaacgctctcggaa (SEQ ID NO:178) caaagtgctgggattacaggcgtga (SEQ ID NO:179)
MitfA			s 25 as 25	ccatgcagtccgaatcggggatcgt (SEQ ID NO:180) ccatctgcatacaggacgctcgtga (SEQ ID NO:181)
Musashi-1		NM_002442	s 26 as 25	caagatgttcatcgggggactcagtt (SEQ ID NO:182) gtacccattggtgaaggctgtggca (SEQ ID NO:183)
Msx-1		M97676	E s 27 (ATG) as 21 (Stop)	gccATGagcttctttgccactcggtgt (SEQ ID NO:184) gacctgggaccctCTAtgtca (SEQ ID NO:185)

Msx-2	S75361	E s 25 (ATG)	accATGgcttctccgtccaaaggca (SEQ ID NO:186)
		as 24 (Stop)	gtcttccTTAggacaggtggtaca (SEQ ID NO:187)
Myt-1		s 24	ggaggtccgctcggatgatgacaa (SEQ ID NO:188)
		as 24	cacgaagcacatgggcctgaggat (SEQ ID NO:189)
Myt-2		s 24	ggacacggtgttgtgctctcagaa (SEQ ID NO:190)
		as 25	cagttacgtggccggttccatcaca (SEQ ID NO:191)
Myt-3		s 26	ggaaccgaggtgccaatggattcact (SEQ ID NO:192)
		as 26	gaagttggagccactgtcccagccat (SEQ ID NO:193)
Nestin	X65964	N s 26	ggcagcgttggaacagaggttgga (SEQ ID NO:194)
		N as 24	ctctaaactggagtggtcagggct (SEQ ID NO:195)
Neuralized-1		s 24 (ATG)	ccaccatgggtaacaacttctccagt (SEQ ID NO:196)
		s-517 23	cccgtcacttctcaccgatgcca (SEQ ID NO:197)
		s-1155 24	ctcggtgagcctatgcgacctcaa (SEQ ID NO:198)
		as-1185 23	ggcacgttgaggtcgcataggct (SEQ ID NO:199)
		as-1932 23	ctcgggcaggctcactggcgaat (SEQ ID NO:200)
		as-2135 24	ctaggagctgcggtaggtcttgat (SEQ ID NO:201)
		as 25 (Stop)	gctaggagctgcggtaggtcttgat (SEQ ID NO:202)
NeuroD1/ Beta2	D82347	s 25	gccccagggttatgagactatcact (SEQ ID NO:203)
		E s 27 (ATG)	ccaacATGaccaaatcgtacagcgaga (SEQ ID NO:204)
		as 25	ccgacagagcccagatgtagttctt (SEQ ID NO:205)
		as E 25 (Stop)	ggtgaaactggcgtgcctCTAatca (SEQ ID NO:206)
NeuroD2			
	AB021742	s 28 (5'UTR)	gtagagatgccacactcgctccgcggtt (SEQ ID NO:207)
	U58681	int as 24	cgatcttggacagcttctgcgtct (SEQ ID NO:208)
		as 23 (Stop)	cggcgcgaagtcTCAgttatgaa (SEQ ID NO:209)
NeuroD3	D81215	s 26 (5'UTR)	gactccaggagacgatgcgacactca (SEQ ID NO:210)
		E s 28 (ATG)	ccgccATGttaacactaccgtttgatga (SEQ ID NO:211)
	U69205	as 25	caagcagcctgccaccaagtttgta (SEQ ID NO:212)
		as 26 (Stop)	gacaggggaggtgaatgaccactgtt (SEQ ID NO:213)
Neurgenin-1	U67777/AC005738	s 24 (5'UTR)	ccggcgacatcactcaggagacca (SEQ ID NO:214)
	U63842	s 26 (ATG)	ctgtccgtcggtcctgcacagcgcaa (SEQ ID NO:215)
		as 24 (Stop)	gtggtaaggaatgaaacagggcgt (SEQ ID NO:216)
Neurgenin-2		s E 26	ccaggatgttcgtcaaatctgagact (SEQ ID NO:217)
		as E 25	cagctctagatacagtccctggcga (SEQ ID NO:218)
Neurogenin-3	AJ133776	s 26 (5'UTR)	cctcgctgctcatcgctctctattct (SEQ ID NO:219)
		E s 26 (ATG)	ccacgATGacgcctcaaccctcgggt (SEQ ID NO:220)
		int as 26	ctgcttgctcagtgccaactcgctct (SEQ ID NO:221)
		as 26 (Stop)	cagcgacagacaggtccttTCAcaga (SEQ ID NO:222)
		E as 26 (Stop)	cagaaaatctgagaaagccagactgcct (SEQ ID NO:223)
Nkx-2B		s 25	ggtctcgaaccatgtcgctgaccaa (SEQ ID NO:224)

		as 24	gggctttgagcgcgtgacatggtt (SEQ ID NO:225)
Nkx-2.5	AB021133	s 25 as 24	cccacgcccttctcagtcaaagaca (SEQ ID NO:226) cgacgccgaagttcacgaagttgt (SEQ ID NO:227)
Nkx-2.8	AF000296	s 25 (5'UTR) as 25 (Stop)	gctaatatcccggctgccagcgcat (SEQ ID NO:228) ctgcggccTCAccagttccaggaga (SEQ ID NO:229)
Noggin	U31202	s 23 (ATG) as 23 (Stop)	gcATGgagcgctgccccagccta (SEQ ID NO:230) cccgagttCTAgcacgagcactt (SEQ ID NO:231)
Nova-1	NM_002515	s 25 (ATG) as 25	cagcggcaggaactgcaaacATGat (SEQ ID NO:232) cagccttcacagtagcacctccctt (SEQ ID NO:233)
Nova-2	AF083898	s 24 as 25 as 25 (Stop)	ggaaccacagagcgggtatgccta (SEQ ID NO:234) cagggagttggtgttgtagccgtaa (SEQ ID NO:235) ggtgacccgctgactgatgaggtat (SEQ ID NO:236)
NSCL-1		s 25 as 25	cagtgacttctagagctcagtggca (SEQ ID NO:237) ccaggcgcagaatctcaatcttgga (SEQ ID NO:238)
NSCL-2		s 24 as 24	ccaagcatctccaagccactgact (SEQ ID NO:239) ccaggacgtggttgagataggaga (SEQ ID NO:240)
Oct-2	XB1030	s 25 as 27	cagtgatctggaggagctggagcaa (SEQ ID NO:241) ggcgatcagcaggatctcctctgaggt (SEQ ID NO:242)
Olf-1		s 25 as 25	cactttgagaagcagccgccttcca (SEQ ID NO:243) ccctatgatgatgacagtcgcacct (SEQ ID NO:244)
Olf-1 Homol		s 25 as 24	gcagcgggctgaacctgaaggagga (SEQ ID NO:245) gggcgtctcattccggttgccaca (SEQ ID NO:246)
Otx-1	AI971638	s 25 as 25	ctagaggacgaggcagagctggaca (SEQ ID NO:247) ccacccagctgttagcatgatgtct (SEQ ID NO:248)
Otx-2	AA334301 AA317337	s 25 as 25	cagacatcttcatgcgagaggaggt (SEQ ID NO:249) gagatggctggtgactgcattggta (SEQ ID NO:250)
Pax-6	NM_000280	s 25 (ATG) as 26	ccagccagagccagcATGcagaaca (SEQ ID NO:251) ggttggtagacactggtgctgaaact (SEQ ID NO:252)
Pbx-1		s 24 as 23	gtagcctttggagatggacgagca (SEQ ID NO:253) ctgcatctggatggagctgaact (SEQ ID NO:254)
Phox2a	AF022722 AF022724	s 23 (ATG) int as 25 as 23 (Stop)	ccgATGgactactcctacctcaa (SEQ ID NO:255) cgtggactccttggaatcgtcgtct (SEQ ID NO:256) gagtggccctgacttggtctcca (SEQ ID NO:257)
Phox2b		s E 36 (ATG)	gcagtatggctgggatggacacctcgagcctggctt (SEQ ID NO:258)
	AB015671	s 24 (ATG) int as 25 as 25 (Stop)	ctccagccaccttctccatatcca (SEQ ID NO:259) gctctcgtcgtccctggaagagtca (SEQ ID NO:260) cgccgcaggattccagaTCAgaaca (SEQ ID NO:261)

		as E 24 (Stop)	gccgcaggattccagatcagaaca (SEQ ID NO:262)
Phox 2b		s E 24 as E 25	ccagtatggccgggatggatacct (SEQ ID NO:263) cgcagatcgcagatcagaacatact (SEQ ID NO:264)
Pitx-3		s E 24 as E 27	ccaccatggagttcggcctgctca (SEQ ID NO:265) cctttccacggcgtactggcacggact (SEQ ID NO:266)
Ptx-3 (mouse)		s E 26 as E 27	ggcatggagtttgggctgcttggtga (SEQ ID NO:267) cacggcgtactggcaggggctaaggtt (SEQ ID NO:268)
RBP-JK		s E 25 as E 24	ggttacatgggactggacagcgcgt (SEQ ID NO:269) ctaagtctggatgaagaggtggaa (SEQ ID NO:270)
REST/NRSF/XBR		s 25 II Fin. as 25 VIII Fin.	gtgaccgctgcggctacaatactaa (SEQ ID NO:271) ggacaagtaggatgcttagatttga (SEQ ID NO:272)
Sall1/Spalt1	Y18264 Y18265	s E 23 (ATG) s 25 int as 24	ccagcATGtcgcggaggaagcaa (SEQ ID NO:273) ggaggaagcaagcgaagcctcaaca (SEQ ID NO:274) cgagttgaggtagagaggttgtga (SEQ ID NO:275)
Sal2/Spalt2	X98834	s 24 s E 29 int as 25 as E 25	gaaagcagcggaaaccccaacagt (SEQ ID NO:276) ccaggatgacttcactaccaagctgggca (SEQ ID NO:277) gcagcacccgtagctcttccaagat (SEQ ID NO:278) ggctcatgggatcgtggggtcatct (SEQ ID NO:279)
Sall3		s E 25 as E 24	cgatcatgaagcaccgcaagggcaa (SEQ ID NO:280) gaacttcttctggcagatggggca (SEQ ID NO:281)
Sharp-1	AW449776 (5') AI819798 (3')	s E 25 (ATG) as E 24	ggaacATGgacgaaggaattcctca (SEQ ID NO:282) caagtggttgatcagctggacaca (SEQ ID NO:283)
Sharp-2/Dec-1	NM_003670	s E 24 (ATG) s 25 as 24 as E 23 (Stop)	ctagtgcagacaggagcgcgcagt (SEQ ID NO:284) gagcacggagacctaccagggatgt (SEQ ID NO:285) cgtgaacctgcgtccgtggtcact (SEQ ID NO:286) gcagcaggatcccctagagagtT (SEQ ID NO:287)
SHH		s 24 as 27	aggatgctgctgctggcgagatgt (SEQ ID NO:288) gccctgctccaggtgcaccgtggccga (SEQ ID NO:289)
Six-3	AF092047	s 29 (ATG) int as 23 as 29 (Stop)	gccATGgtattccgctcccccctagacct (SEQ ID NO:290) gcctggtgctggagcctgttctt (SEQ ID NO:291) ggCTAtcatacatcacattccgagtcgct (SEQ ID NO:292)
SMAD-6	AF035528	s 29 (ATG) as 26 (Stop)	cgtATGttcaggtccaaacgctcggggct (SEQ ID NO:293) ccgccaCTAtctggggttgttgagga (SEQ ID NO:294)
SMAD-7	AF010193	s 24 (ATG) as 24 (Stop)	ccccgcATGttcaggaccaaacga (SEQ ID NO:295) cacgcggctaccggctgttgaaga (SEQ ID NO:296)

Sox-1	X13436	s 26 (ATG)	cccgATGtacagcatgatgatggaga (SEQ ID NO:297)
		as 26	gtacatgctgatcatctcgcgcaggt (SEQ ID NO:298)
Sox-2		s 26 (ATG)	gccATGtacaacatgatggagacgga (SEQ ID NO:299)
		as 25 (Stop)	cctccagttcgctgtccggcccTCA (SEQ ID NO:300)
Sox-3	X71135	s 25 (ATG)	caggcagactgtgaATGcgacctgt (SEQ ID NO:301)
		as 26 (Stop)	cTCAgatgtgggtcagcggcaccgtt (SEQ ID NO:302)
Sox-10	AJ001183	s 25	gtgggcgttggactctttgcgagga (SEQ ID NO:303)
		s E 25 (ATG)	gcgacATGgcggaggagcaggatct (SEQ ID NO:304)
		int as 26	gctggtacttgtagtccgggtggtct (SEQ ID NO:305)
		as 24 (Stop)	cctTTAgggccgggacagtgtcgt (SEQ ID NO:306)
		as E 26	cacgttgccgaagtcgatgtgaggct (SEQ ID NO:307)
Sox-11		s 24	ggatcatggtgcagcaggcggaga (SEQ ID NO:308)
		as 25	ccagaaacacgcacttgaccgtctt (SEQ ID NO:309)
Synemin		s 25	gcgattgactgcctggaggatgaga (SEQ ID NO:310)
		as 25	cgaagcacctgctgccaccttgtct (SEQ ID NO:311)
TAF135	Y11354	s-1 26	ctggacgaggtcttcttcaacagcga (SEQ ID NO:312)
		s-2 25	ggaatggtcctcgtccgaagtgaga (SEQ ID NO:313)
		as-1 25	gcatagttggcccgatgaccatgct (SEQ ID NO:314)
		as-2 26	gggtaagctcctcttcaggaaaggca (SEQ ID NO:315)
		as-3 24	ggtaacacggcgggtttcaccaca (SEQ ID NO:316)
		as-4 25	gcctgctcatatctgtcgtcatcct (SEQ ID NO:317)
		as-5 24	gtagagcagcagtgaatggcttgt (SEQ ID NO:318)
TBP		s-1 25	ggatcagaacaacagcctgccacct (SEQ ID NO:319)
		as-1 26	gcggtacaatcccagaactctccgaa (SEQ ID NO:320)
		as-2 26	ggcacgaagtgcaatggtctttaggt (SEQ ID NO:321)
		as-3 26	cgtggttcgtggctctcttatcctca (SEQ ID NO:322)
		as-4 27	cttcacatcacagctccccaccatgtt (SEQ ID NO:323)
		as-5 26	ggaggcaagggtacatgagagccatt (SEQ ID NO:324)
TRAP80/ CRSP77	AF117657	s-1 24	ccagtctgagcgttgcgttcggtt (SEQ ID NO:325)
		s-2 24	ggccttgggactcagtgaggaaca (SEQ ID NO:326)
		as-1 25	cgtctgaggattctgttttggagga (SEQ ID NO:327)
		as-2 28	ctcggaaagggctgagagataatctggt (SEQ ID NO:328)
		as-3 24	cggcttgctaagctgtcaatggtt (SEQ ID NO:329)
		as-4 24	gtagacaagggctaagtgcagaca (SEQ ID NO:330)
TRAP170/ EXLM1/ CXORF4/ CRSP150	AF135802	s-1 25	gtgttgacggacctactgccaagga (SEQ ID NO:331)
		s-2 24	ggtatcatgctggaaagtgcctct (SEQ ID NO:332)
		s-3 24	gccaagcgcaagttgtctgatgat (SEQ ID NO:333)
		s-4 26	cgttctctaccagacatacctgctca (SEQ ID NO:334)
		s-5 24	gcagccaggaacatcaggtgctta (SEQ ID NO:335)
		as-1 25	gggagtgcagtctctatggaagagt (SEQ ID NO:336)

		as-2 26	caccttccacttgcactccttgatgt (SEQ ID NO:337)
		as-3 25	gtggacgactgtggcagaatggaga (SEQ ID NO:338)
		as-4 26	ggtcaagagttccatgtggactagca (SEQ ID NO:339)
		as-5 26	ctgctgtctgggaatgtctgcctgct (SEQ ID NO:340)
Xanf-1/Hesx1		s 25 (ATG)	ccacgagaggATGtctcccagcctt (SEQ ID NO:341)
		as 25	cgataccaggatagcagtttactct (SEQ ID NO:342)
Zic-1	D76435	s E 28	ccacgatgctcctggacgccggcccccca (SEQ ID NO:343)
		s 24	cggagcagtacggccaggtgacca (SEQ ID NO:344)
		as 26	gattcgcagggttctttcagtaatgt (SEQ ID NO:345)
		as E 26 (Stop)	gattcgcagggttctttcagtaatgt (SEQ ID NO:346)
Zic-2	AF104902	s 24	cgccgagatgcaggaccgtgaact (SEQ ID NO:347)
		as 24	ggaggtgtggacgtgcatgtgctt (SEQ ID NO:348)
Zic-3		s 23 (ATG)	gccATGacgatgctcctggacgg (SEQ ID NO:349)
		as 23 (Stop)	ccTCAgacgtaccattcgttaaa (SEQ ID NO:350)
Ku p70/p80		s E 24	cggcaacatggtgcggtcggggaa (SEQ ID NO:351)
		as E 29	ccaacatggtgcggtcggggaataaggca (SEQ ID NO:352)
MRE11		s E 28	ccaccatgagtactgcagatgcacttga (SEQ ID NO:353)
		as E 28	cctgtatcttgcatgtttctcagggcca (SEQ ID NO:354)
NBSI/nibrin		s E 19	ccacgatgtggaaactgct (SEQ ID NO:355)
		as E 24	gcctgaagtagatgcttactagga (SEQ ID NO:356)
PCNA		s E 25	gttgttgccactccgccaccatgtt (SEQ ID NO:357)
		as E 26	gcctaagatccttcttcatcctcgat (SEQ ID NO:358)
PIR51		s E 30	cgaccatggtgcggcctgtgagacataaga (SEQ ID NO:359)
		as E 24	ccacactcaggtgctagtggcatt (SEQ ID NO:360)
RAD51B		s E 29	ccagcatgggtagcaagaaactaaaacga (SEQ ID NO:361)
		as E 25	ctgtctctaggaatttccataggct (SEQ ID NO:362)
RAD52		s E 26	gcaagatgtctgggactgaggaagca (SEQ ID NO:363)
		as E 26	gtggcctgagcctcagtaagatggat (SEQ ID NO:364)
RAD54B		N s E 25	ggcgcgctaacgacgttcctaacaa (SEQ ID NO:365)
		as E 26	cactatgtgccagtagcttgagtggt (SEQ ID NO:366)
RFC 40 kD		s E 26	cgagaatggaggtggaggccgtctgt (SEQ ID NO:367)
		as E 24	gtcagtcagtgaagtctctgctct (SEQ ID NO:368)
RFC 140 kD		s E 28	ccacgatggtgccctccagcccagcggt (SEQ ID NO:369)
		as E 24	gcccgagagtcactggttcacatt (SEQ ID NO:370)

RPA 14kD	s E 30	ccagcatggtggacatgatggacttgccca (SEQ ID NO:371)
	as E 24	gatcaatcatgttgcacaatccct (SEQ ID NO:372)
RPABCA	s E 27	cgaccatggagggaggcttgaagagga (SEQ ID NO:373)
	as E 26	ccctctatcacagttttaggacccca (SEQ ID NO:374)
XRCC2	s E 24	ccgcgatgtgtagtgccttccata (SEQ ID NO:375)
	as E 24	gcgtagtaccctgcaaaagactat (SEQ ID NO:376)
XRCC3	s E 30	gcaccatggatttggatctactggacctga (SEQ ID NO:377)
	as E 27	gtgttgtgcagccgccaccgtgtcagt (SEQ ID NO:378)
XRCC4	s E 26	ccaccatggagagaaaaataagcaga (SEQ ID NO:379)
	as E 27	ctcatcaaagaggtcttctgggctgct (SEQ ID NO:380)

Methods of Diagnosis and Treatment

[0060] Development of tumor classifications based on the neoplastic molecular marker expression patterns has an important heuristic value. It allows practitioners to identify the molecular profile of a subject's tumor cell and diagnose the type of cancer with which the subject is afflicted.

[0061] Accordingly, in some embodiments, the disclosed methods are useful for diagnosing the existence of a neoplasm or tumor of any origin. For example, the tumor may be associated with carcinoma, astrocytoma, sarcoma, retinoblastoma, melanoma, Wilm's tumor, bladder cancer, breast cancer, colon cancer, hepatocellular cancer, pancreatic cancer, prostate cancer, lung cancer, liver cancer, stomach cancer, cervical cancer, testicular cancer, renal cell cancer, and brain cancer. In preferred embodiments, the tumor is a neural cell tumor, lung tumor or prostate tumor.

[0062] Early and effective diagnosis of various tumor types would be a great boon to the treatment of various neoplastic diseases. Such identification capabilities would permit practitioners to fashion highly specific cancer treatments based upon the identification of the individual tumor type.

Development of a Database

[0063] The diagnosis and ultimate treatment of neoplastic disease based upon molecular markers produced directly or indirectly from a neoplastic cells is facilitated by the

development and utilization of a database correlating neoplastic molecular characteristics (TAA or TAB profiles) with specific tumor sub-types. Based upon the classification of the neoplasm, treatment modalities can be proposed. Thus, in one embodiment of the disclosed invention, a database of molecular characteristics of tumor-associated antibodies (TABs) and tumor-associated antigens (TAAs) is provided.

[0064] A database of molecular characteristics of different tumors and TABs has been developed that provides information regarding a specific treatment for individual tumors based on the neoplastic molecular marker characteristics of a tumor. Namely, the database relates the molecular description of a tumor; the response of tumor cells to various stimuli; and the profiles of antibodies against TAAs in a subject's blood based upon the specific neoplastic molecular markers. The classification is made possible, in part, because each tumor cell and its attendant set of TAAs has a predictable expression pattern of regulatory genes that is reflected in the blood profile of TABs.

EXAMPLES

Molecular Classification of Specific Tumors

[0065] The examples below demonstrate the molecular classification of specific types of tumors or neoplasms. Specific classes of tumors are subdivided into subclasses based upon gene expression profiles of regulatory factors at the mRNA and protein levels. The analysis below shows that using expression profile of transcriptional regulators in biopsy material or bodily fluids and/or blood profile of antibodies against specific transcriptional regulators allows to classify variety of tumor types into molecular subclasses. These subclasses are used for diagnostic purposes. Additionally, the tumor types classified below have been shown to demonstrate specific responses to a variety of treatments.

[0066] The list of neoplastic molecular marker used in the following examples is not finite. Using the methods disclosed herein, additional factors can be added to the arrays illustrated below to expand the classification system and to increase its specificity. Notwithstanding the expandability of the methods disclosed herein, the addition of new neoplastic molecular markers to the system does not alter the basic principle of the disclosed invention.

[0067] Tumors that develop from early stages of neural lineage (*e.g.*, stem cells), express early markers of neurogenesis, such as helix-loop-helix (HLH) transcription factors of the neurogenin family, zinc finger transcription factors of the Zic family, high mobility group transcription factors of Sox family, homeodomain transcription factors of the Emx family, and a large number of other transcription factors that are involved in suppressing neural development, such as the HLH transcription factors of the HES family, homeodomain transcription factors of the MSX family, and inhibitory SMAD transcription factors. By contrast, tumors that develop from more differentiated neural cells express genes that are characteristic for this type of neoplasms. Late expressed homeodomain transcription factors of the LIM family, HLH transcription factors, and zinc finger transcription factors are all examples of transcription factors expressed in more differentiated neural cells.

Example 1

Gene Expression Profiling Of Astrocytomas

[0068] The data presented in this example relates to the classification of astrocytomas. Diffuse, fibrillary astrocytomas are the most common neural tumors. They are typically divided into three grades of malignancy: World Health Organization (WHO) grade II astrocytoma, WHO grade III anaplastic astrocytoma and WHO grade IV glioblastoma multiforme (GBM). The WHO classification system is primarily based on morphological criteria and does not reflect the molecular nature of glioma cells. By contrast, the molecular classification provided by the described methods is based upon the expression of transcription factors in tumor cells.

[0069] Biopsy material from 11 patients with different grade astrocytomas was analyzed using different antibodies against transcription factors (tumor-associated antigens) that are characteristic for the early development of the nervous system. The results of this work are shown in Table 9.

[0070] The results shown in Table 10 were generated by applying general immunohistochemical techniques. Specifically, tissues were obtained, dissected, and immediately frozen on dry ice. Sections of 10 μm thick were obtained using a cryostat. Dissected tissue on slides was dried at room temperature for 30-90 minutes and then fixed with cold acetone/methanol (50/50) 2 minutes. Once dried, the slides were then treated with

0.05% trypsin for 10 minutes at 37°C, and then washed three times with phosphate buffered saline (PBS). The slides were then air-dried slides and washed with PBS for 5 minutes. The dried slides were then incubated in 50 mM ammonium chloride for 30 minutes, followed by a wash with PBS for 5 minutes. Non-specific binding was blocked by incubating the slides in a Tween/bovine serum albumin (BSA) solution for 30-45 minutes. Following the blocking step, the slides were incubated with a primary antibody specific for the indicated neoplastic molecular marker for 90 minutes at dilutions ranging from 1:100 - 1:600. The antibodies utilized were either commercially available or generated using standard techniques. Unbound primary antibodies were removed from the slides with washes performed three times for 5 minutes each using PBS. Following these washes, the slides were incubated with a secondary fluorochrome-conjugated antibody for 30 minutes. The slides were then washed four times for five minutes each in PBS. After the last wash the slides were mounted. The results of this work is shown below.

Table 10

Astrocytoma-specific profiling

	S1	S2	S3	GM1	GM2	GM3	GM4	AA1	AA2	AA3	AA4	AA5	AG1	AG2
NGN1	-	-	-	?	+	+	+	+	?	+	+	-	-	-
NGN2	+	+	+	+	+	+	+	+	+	+	+	-	+	+
NeuroD1	+	+	+	+	+	+	+	-	+	+	+	+	+	+
NeuroD2	+	-	-	+	-	+	-	-	+	-	-	-	+	-
ATH1	-	-	-	+?	+	+	+	-	+?	+	-	-	-	-
ATH5	+	+	+	+	+	+	+	+	+	+	+	+	+	+
ASH1	-	-	-	-		-		+	-	-	-	-	-	
NSCL2	-	-	-	+	-		-	-	+	-	-	-	-	-
HES2	+	+	+	+	+?	+	-	-	-	+	+	+	-	-
SHARP1	+	+	+	+	+	+	+	-	+	+	+	-	+	-
Hey1/HRT1	+	+	+	+	-	+	-	-	-	+	+	+	-	-
Hey2/HRT2	+	+	+	+	+	+	+	-	+	+	+	+	+	+
HeyL/HRT3	+	+	+	+	-	+	-	-	+	+	+	-	+	-
Groucho1	-	+	-	-	-	-	-	-	-	+	-	-	-	-
Groucho3	-	-	-	-	+	-	+	-	+	+	+		+	-

	S1	S2	S3	GM1	GM2	GM3	GM4	AA1	AA2	AA3	AA4	AA5	AG1	AG2
Groucho4	+	-	-	-	-	-	-	-	+	+	+	+	+	-
EN1	-	+	+	-	+	-	+	-	+	+	-	-	-	-
EN2	-	-	-	-	-	-	-	+	-	-	-	-	-	-
SOX1	+?	-	-	+	+	+	+	-	-	+	-	-	-	-
SOX2	+	+	+	+	+	+	+	+	-	-	+	+	-	-
SOX3	+	+	-	+	+	+	+	+	+	+	+	-	+	+
SOX10	+	+	+		-		+	-	-	+?	+	+	-	-
Sal2	+	+	-	-	-	-	-	-	-	+	+	-	-	-
Sal3	-	-	-	-	-	-	-	-	+	-			-	-
PTX3	-	-	+	-	+	+	+	-	-	+	-	-	-	+
NOT1	-	-	-	-	+	-	+	-	-	+	-	-	-	-
Isl1	+	+	+	-	+	+	+	+	+	+	+	+	+	+
LHX2	-	-	-	-	+	-	+	-	-	+	+	-	-	-
LHX3	-	-	-	-	-	-	-	-	-	+	-	-	-	-
LMO4	-			+	-	+	-	-	+	+	-	-	+	-
NKX2.2	+	-	-	-	-	-	-	-	-	-	-	-	-	-
NKX2.9	+	-	-	-	-	-	+	-	-	+	-	-	-	-
NKX5.2	+	-	+	+	-	+	-	+	+	+	+	+	+	+
GBX2										+				-
Brn5	+	+	+	+	-	+	+	+	+	-	+	+	+	+

[0071] Abbreviations to Table 10: S, control subject; GM, glioblastoma multiforme; AA, grade 2 astrocytoma; AG, anaplastic glioma; numbers refer to different subjects; +, expressed; -, not expressed; +?, unable to identify/detect; empty – no data.

[0072] The analysis of these results demonstrate that individual tumors express unique sets of transcriptional regulators. For example, the characteristic differences of glioblastomas multiforme (GM) compared to anaplastic gliomas (AG) and grade 2 astrocytomas (AA) is the expression of Sox family of transcription factors.

Identity of Subclasses of Glioblastoma Multiforme tumors

[0073] Five distinct subclasses of glioblastoma multiforme tumors were identified as follows: Subclass I: High expression of negative regulators of neural differentiation such

as Msx genes and no expression of neuronal genes such as Neurogenins, Emx-s and Lim-s and negative regulators of HES family. Subclass II: High expression of HES genes and TGFβ signaling cascade molecules (SMADs), no neuronal genes. Subclass III: High expression of HES genes and neural genes of Neurogenin, NeuroD and ASH family. Subclass IV: High expression of HES genes and homeodomain genes of Lim and Emx family, no expression of NeuroD and ASH family HLH transcription factors. Subclass V: Moderate expression of HES and Msx family genes, no expression of neural homeodomain genes.

Example 2

Antibodies Against Transcription Factors In The Blood Of Subjects With Small Cell And Non Small Cell Lung Cancer – A Clinical Study

[0074] Lung cancer is one of the most common neoplastic diseases in the United States, representing about 15% of all cancer cases and accounting for over one-fourth (28%) of cancer deaths in the United States (Hammar, 1994). It is the number one killer by cancer and in fact, kills more people than colon, prostate and breast cancer combined. Lung cancer is especially common among men in North America, Europe, and Oceania. There are many types of lung cancer, but most can be categorized into two basic types, small cell and non-small cell. Non-small cell lung cancer (NSCLC) that develops from lung neuroendocrine (NE) cells is a heterogeneous group of 3 clinically distinct types of tumors, including large cell carcinoma, and typical and atypical carcinoids. 80% of all lung tumors are diagnosed as NSCLCs. Carcinoids represent a rare group of tumors of NE system accounting for 1% to 3% of all lung tumors.

[0075] Identification of SCLC and NSCLC using auto-antibody profile from an afflicted subject's blood allows for noninvasive diagnosis of lung cancer. SCLC is characterized by the presence of the following set of antibodies against transcription factors NeuroD2, ATH5, Sox1, Sox2 and LMO4. When blood contains antibodies against these transcription factors then lung cancer patient has 80% probability to have SCLC. NSCLC is identifiable by the Groucho1, Sox2, Sox3 and Nkx5.2 antibodies.

[0076] Blood from 4 non-cancer patients, 7 patients diagnosed with well-developed small cell lung cancer (SCLC), and 8 patients diagnosed with well-developed non-

small cell lung cancer (NSCLC) was used to identify diagnostic markers for the molecular distinction of the SCLC and NSCLC disease states. The blood sera from these individuals was dot blot analyzed for the presence of transcription factor-specific TABs.

[0077] This analysis showed that these two tumor types are well-discriminated by different sets of diagnostic markers in the blood (Table 11). The analysis of this data indicates that the SCLC neoplastic disease state is characterized by the presence antibodies against transcription factors NeuroD2, ATH5, Sox1, Sox2, and LMO4 in the subject's blood. The NSCLC neoplastic disease state is characterized by the presence of antibodies against HeyL/HRT3, Sox1, Sox2, and Nkx5.2.

Table 11

Lung Cancer-Specific TAB Profile

	control				SCLC							NSCLC							
	1	2	3	4	1	2	3	4	5	6	7	1	2	3	4	5	6	7	8
NGN1	+																		
NGN2					+	+	+		+						+				
NGN3																		+	
NeuroD1					+														
NeuroD2					+	+	+	+	+	+	+				+			+	
NeuroD3																			
ATH1								?											
ATH5					+	+	+		+	+	+				+			+	
ASH1																			
NSCL1		+																	
NSCL2						+		+							+				
HES1																			
HES2					+			+	+				+						+
HES3																			
HES5																			
SHARP1					+						+								
SHARP2																			
Hey1/HRT1																			

	control				SCLC							NSCLC							
	1	2	3	4	1	2	3	4	5	6	7	1	2	3	4	5	6	7	8
Hey2/HRT2		+																	
HeyL/HRT3												+			+	+	+	+	
Groucho1							+			+				+					
Groucho2																			
Groucho3																			
Groucho4																			
EN1			+																
EN2																			
SOX1					+	+	+		+		+		+	+	+		+		+
SOX2			+		+	+	+		+		+			+	+	+	+		
SOX3																			
SOX10							+	+		+		+				+		+	
SOX11							+			+						+		+	
RBP-Jk																			
Sall1									+		+		+		+				+
Sal2						+													
Sal3																			
Phox2A	+							+								+			
Phox2B																	+		
PTX3				+															
NOT1																			
Isl1						+	+			+						+			
LHX2					+				+					+			+		
LHX3																			
LHX4																			
LHX5																			
LMO4						+	+	+		+	+				+				
NKX2.2																			
NKX2.9																			
NKX.5.1																			+

	control				SCLC							NSCLC							
	1	2	3	4	1	2	3	4	5	6	7	1	2	3	4	5	6	7	8
NKX5.2												+	+	+		+	+		
DLX1																			
DLX2																			
DLX5																			
GBX2						+				+	+				+				
Brn5							+				+				+			+	

[0078] Abbreviations to Table 11: control, control subject; SCLC, small cell lung cancer; NSCLC, non-small cell lung cancer; numbers refer to different subjects; +, expressed; ?, not able to identify/detect; empty, not expressed.

Example 3

Profile of Auto-Antibodies Against Transcription Factors In The Blood Of Subjects With Prostate Cancer: A Clinical Study

[0079] Prostate cancer is the most common form of neoplastic disease in men. Prostate cancer is the second leading cause of cancer death after lung cancer. 80% of men over the age of 65 who have cancer have prostate cancer (data of American Cancer Society). One in five men will develop prostate cancer in their lifetime. Next to age, race tends to be important cause of this cancer, since African-American males have the highest rate of prostate cancer in the world, and they tend to be diagnosed at late stage. Adenocarcinoma of the prostate is one of the most common tumors in men and accounts for 10% of deaths from malignant disease in males in the United States. Only a small proportion of these cases becomes clinically apparent prior to death, the remainder being latent carcinoma. Although some immunological diagnostic assays are available, the only reliable procedure for definitive diagnosis of prostatic carcinoma is by open perineal biopsy. Needle biopsies and cytologic studies of prostatic fluid are unreliable for the diagnosis of early cancer but are useful methods of obtaining a histological diagnosis in the more advanced cases.

[0080] To evaluate presence of TABs against transcriptional regulators in patients' blood as a diagnostic marker for molecular subgroups of prostate cancer, the blood serum of 10 noncancer patients and of 21 patients diagnosed with well-developed tumors was

analyzed. It was established that these tumors exhibited neuroendocrine-like differentiation by examining the levels of chromogranin A in the blood sera, which were exceedingly higher in the blood of patients with cancer than in the sera of the control group. Blood samples were collected during the period of 1990-1995, aliquoted and stored at –80 °C. None of the samples had been previously thawed. All patients with prostate cancer have been receiving treatment, either androgen ablation therapy or radiotherapy.

[0081] Peptides (see Tables 1-8) in the concentration of 1 mg/ml (H_2O) were blotted in 0.25 µl volumes onto nitrocellulose filter. The dried filter was exposed to a blocking solution (PBS, 1% Tween 20, 1% casein, 1% goat serum; and 5mM EDTA) overnight at 4°C. After four washes with PBS, 0.1% Tween 20, the filter was incubated with goat anti-human Ig-conjugated to alkaline phosphatase secondary antibody (Dako) which had been diluted 1:1000 in the blocking solution. After four washes with PBS, 0.1% Tween 20, color reaction for peroxidase was performed using a mix of diaminobenzidine (DAB, Sigma –D-5637; 10 mg in 5 ml methanol) and chloronaphtole (30 mg in 5 ml methanol) as a substrate. Each time a fresh substrate solution (0.5 ml of DAB stock + 0.5 ml chloronaphtole stock + 4 ml PBS + 5 microliters of H_2O_2) was made. Finally, densitometric analyses or alternatively qualitative evaluation of the filters was performed to determine the presence or absence of a signal on the blot.

Table 12

Profile of Auto-Antibodies Against Transcription Factors In The Blood Of Subjects With Prostate Cancer

	control patients										Prostate carcinoma patients																				
	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
NGN1											1								1							1			1		
NGN2							1				1	1					1				1						1			1	1
NGN3													1						1	1						1			1		
NeuroD1												1							1									1			
NeuroD2			1								1	1			1	1	1				1	1	1	1	1			1		1	1

	control patients										Prostate carcinoma patients																				
	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
NeuroD3																															
ATH1											1	1		1	1	1			1	1		1	1	1				1		1	
ATH5											1	1	1	1	1	1		1	1	1		1	1	1	1	1	1	1		1	1
ASH1																															
NSCL1																															
NSCL2																	1											1			
HES1																															
HES2											1		1		1	1		1		1	1		1		1	1			1	1	
HES3				1		1						1																			
HES5																															
SHARP1													1				1	1			1				1	1	1				1
SHARP2													1												1		1				
Hey1/HRT1																															
Hey2/HRT2																															
HeyL/HRT3														1	1	1							1								
Groucho1																															
Groucho2																	1														
Groucho3																											1				
Groucho4																															
EN1		1								1																					
EN2																															
SOX1											1		1		1	1		1		1	1		1		1	1	1		1	1	
SOX2			1					1			1	1	1		1	1	1	1	1		1		1	1			1	1			1
SOX3														1			1	1				1			1	1	1		1	1	
SOX10											1									1						1					1
SOX11																															
RBP-Jk																															
Sall1													1				1	1				1			1	1	1		1		1
Sal2																															
Sal3																															
Phox2A	1																														

	control patients										Prostate carcinoma patients																				
	1	2	3	4	5	6	7	8	9	10	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
Phox2B																															
PTX3											1	1												1							
NOT1							1																								
Isl1											1	1		1	1	1			1	1		1	1	1				1		1	
LHX2																															
LHX3												1	1	1			1			1			1	1	1				1		
LHX4					1																										
LHX5																															
LMO4											1	1		1	1	1			1	1		1	1	1						1	
NKX2.2													1				1	1							1	1	1		1		
NKX2.9																															
NKX.5.1																															
NKX5.2																															
DLX1																															
DLX2																															
DLX5																															
GBX2			1				1				1	1		1	1	1			1	1		1	1	1				1		1	
Brn5												1	1		1			1			1	1	1	1		1	1				1

[0082] Abbreviations to Table 12: numbers in the top row of the Table refer to different subjects; 1, presence of the TAB; empty, absence of the TAB.

[0083] Based on the presence of TABs in the blood of the patients diagnosed with prostate carcinoma, two subgroups of patients were identified. Group I typically had antibodies against: NeuroD2, ATH1, Isl1, LMO4, GBX2, including patients 1,2,4,5,6,9,10,12,13,14,18,20. Five of them (41.6%) are dead already. Group II had antibodies against: Nkx2.2, Sall1, Sharp1; including patients 3,7,8,15,16,17,19. In this group only one patient (14.3%) has died. Based on the survival data, it was also observed that patients with prostate carcinoma of group II respond better to hormone and radiotherapy.

<u>Example 4</u>

Gene Expression Profiling Of Neuroblastomas

[0084] The expression of various regulatory genes expressed at early stages of neurogenesis were examined in five different human neuroblastomas. All neuroblastomas exhibit expression of a variety transcription regulatory factors that demarcate the highly mitotic active region in the nervous system - the subventricular zone. However, neuroblastomas can be clearly identified by the presence and extent of different signaling pathways that are implicated during neurogenesis, particularly by the presence of molecular markers such as BMP/TGFβ, SHH, and Notch. Furthermore, in different neuroblastomas proneural genes ASH-1 and Neurogenin1 are expressed in complementary fashion. In addition, several other bHLH genes (*e.g.*, Hes5, Hey1, NeuroD1, NeuroD2, and NeuroD3(6)) exhibit similar neuroblastoma-specific restriction, as do Neurogenin1 and ASH1, forming the signatures for the molecular classification of neuroblastomas.

[0085] Briefly, the expression of various transcriptional regulatory factors in different human neuroblastomas was examined using RT-PCR analysis. First strand cDNAs were synthesized with reverse transcriptase (Superscript^{II}, Life Technologies Inc.) using 5-10 μg of mRNA from different cell lines as a template. PCR reactions were performed in the volume of 25μl containing 1/10 of RT reaction as a template and GC-Rich PCR System or the Expand^{TM} Long Distance PCR System kit (Roche) according to manufacturer's instructions. DNA was amplified using in most cases the following conditions: 94°C (2min); 35-40 cycles of 94°C (30s), 56°C (40s), 72°C (150s). For all combinations of primers, the annealing temperature and the number of cycles was optimized beforehand. All amplified PCR products were sequenced to rule out false positives using *fmol*® DNA Cycle Sequencing System (Promega. The amplified RT-PCR products were resolved on 1.0-1.2% agarose gel.

Table 13

RT-PCR Analysis of Neuroblastomas

	control						GDNF+TGFβ1				
	1	2	3	4	5		1	2	3	4	5
Gata-2	1	1	1	1	1		1	1	1	1	1
Gata-3	1	1	1	1	1		1	1	1	1	1
Pbx-1	1	1	1	1	1		1	1	1	1	1
LMO4	1	1	1	1	1		1	1	1	1	1
Sox2	1	1	0	0	0		1	1	0	0	1

Sox11	1	1	1	1	1		1	1	1	1	1
Bmp-2	1	1	0	0	0		1	0	0	0	0
Bmp-6	1	1	0	0	0		1	1	0	0	0
noggin	1	1	0	0	0		1	1	0	0	0
chordin	1	1	0	0	0		1	0	0	0	0
SMAD6	1	1	0	0	0		1	0	0	0	0
SMAD7	1	1	1	1	1		1	1	1	1	1
Msx1	1	1	0	0	0		1	1	0	0	0
Msx2	1	1	0	0	0		1	1	0	0	0
Gli1	1	1	0	0	0		1	1	0	0	0
Gli2	1	1	1	1	1		1	1	1	1	1
Gli3	1	1	0	1	0		1	1	0	1	0
Zic1	1	0	0	0	1		1	0	0	0	0
Zic2	1	1	0	0	0		1	1	0	0	0
Zic3	1	0	0	0	0		1	0	0	0	0
Irx2a	1	1	1	1	1		1	0	0	1	1
Irx3	1	0	1	0	0		0	0	0	0	0
NN1	0	0	0	0	0		0	0	0	0	0
NN3	0	0	1	0	0		0	0	1	0	0
Ash-1	0	0	1	1	1		1	1	1	1	1
Olf-1	1	1	1	1	1		1	1	1	1	1
Olf-1H	1	1	1	1	1		1	1	1	1	1
NeuroD1	0	0	1	1	1		1	1	1	1	1
NeuroD2	1	1	1	1	1		1	0	0	0	0
NeuroD3	1	1	0	0	0		1	1	0	0	0
NSCL1	1	1	1	1	1		1	1	1	1	1
NSCL2	1	1	1	0	0		0	0	0	0	0
Hes-1	1	1	1	1	1		1	1	1	1	1
Hes-5	0	0	1	1	1		0	0	1	1	1
Hey1	0	0	1	1	1		1	1	1	1	1
Hey2	1	1	1	0	0		1	1	1	1	1
HeyL	1	1	0	1	0		1	0	1	1	0
MyT-1	0	1	1	1	1		0	1	1	1	1
MyT-2	0	0	1	0	1		0	1	0	0	1
MyT-3	0	0	0	0	0		0	0	0	0	0
Otx1	1	1	0	0	0		0	1	1	1	1
Otx2	1	0	0	0	0		0	0	0	0	1
Pax6	1	1	0	0	0		1	0	0	0	0
Brn4	1	1	1	1	1		0	0	0	0	1
Brn5	1	1	1	1	1		1	1	0	0	0
Dlx2	1	1	0	0	0		1	1	1	1	1
Dlx7	1	1	1	1	1		1	1	0	1	0
Nkx2.5	0	1	1	1	0		1	1	1	1	1
Neu	0	0	1	1	1		1	1	1	1	1

Med6	1	1	1	1	1		1	1	0	0	0
GFAP	0	0	0	0	1		1	1	1	1	1
βIIItub	0	0	1	0	1		1	1	1	1	1

N.B.: The numbers in the top row of the Table refer to different subjects; a "1" value refers to mRNA expression; and a "0" value connotes no expression of mRNA.

[0086] The effect of growth factors on the proliferation and differentiation of five human neuroblastomas (Table 14) was also examined. The data established that transcriptional regulatory factor networks operational in human neuroblastoma cells are involved in neural differentiation of human neuroblastoma cells in response to growth factor treatment. The change in expression patterns of transcriptional regulatory factors upon growth factor-treatment of neuroblastomas is compared to the extent of neural differentiation of these tumor cells as examined by the expression of various neural-specific markers. Two major adaptations were observed in the TF networks of NBs upon GF (GDNF and TGFβ1) treatment. The first adaptation included genes that exhibited cell-autonomous regulation and showed no change in their expression upon treatment. This group of genes comprised mostly of early negative regulators and TFs characterizing the fate switches to specific neural lineages. The second adaptation included genes that exhibited signal-dependent regulation and their expression was affected by GF treatment. This group comprised mostly of TFs associated with specification of neuronal identity, e.g proneural and neurogenic genes. Ultimately, using cluster analysis methods, we demonstrated that information relevant to NB classification that considers cellular potential of a tumor for GF-induced differentiation can be reduced to distinct sets of at least 5 transcription regulators which are implicated in neurogenesis. These observations suggest a basic strategy for NB diagnostics and therapeutics whereby a relatively small number of TFs, which are followed as identifiers of development and cell function, could be used to classify tumors according to their cellular potential for differentiation.

[0087] Results of the analyses demonstrate that neuroblastomas have specific responses to growth factors, and likely this response depends on the expression profile of regulatory factors which can be exploited as a prognostic marker for therapeutic outcome.

Table 14

The effect of GDNF and TGFβ1 on the proliferation of neuroblastomas

	1	**2**	**3**	**4**	**5**
TGFβ1/ GDNF	3.6↑	3.6↓	2.3↑	NE	NE

[0088] Human NB cells were grown for 6 days on laminin-coated 24-well plate in DMEM/F-12/B27 media in the presence of GDNF (100ng/ml) and TGFβ1 (100ng/ml). After 6 days cells were dissociated and an aliquot of cells was counted using hemocytometer. Values represent the relative change (in folds) in cell number normalized to the relative change in cell number of GF-untreated cultures. Abbreviations: NE, -no effect in comparison with control; ↑ - enhanced proliferation in comparison with control; ↓ - reduced proliferation in comparison with control.

[0089] These data indicate that individual neuroblastomas reflect a certain stage of neural development, characterized by the expression of stage-specific regulatory genes. These observations suggest a basic strategy for neuroblastoma diagnostics and therapeutics whereby a relatively small number of transcriptional regulatory factors, which are followed as identifiers of cell function and development, could be used to monitor and promote cellular potential for differentiation in tumors.

Example 5

Gene Expression Profiling Of Non Small Cell Lung Cancer

[0090] Gene expression profiling of NSCLC cells was performed using RT-PCR techniques, establishing that individual NSCLCs reflect a certain stage of neural development, characterized by the expression of stage-specific regulatory genes, and revealing that Zic family of TFs, MyT-2, Hes-5, SMAD6 forming the signatures of the molecular marker-based classification of carcinoids.

[0091] Total RNA was isolated from 500,000 cells using an acid-phenol extraction method as described Timmusk et al., Neuron *10(3)*, 475- 489 (1993). RT-PCR analyses was performed as detailed in Palm et al., Brain Res. Mol. Brain Res. *78(1-2)*, 192-195 (2000) using 45 cycles in each amplification. Primer sets were designed in a manner that sense and antisense primers recognized different exons facilitating the discrimination between RT-PCR amplification products of genomic DNA and mRNA. (Table 9). All amplified PCR products were sequenced to rule out false positives. The results from this work are shown in Table 15.

Table 15

RT-PCR Analysis of NSCLC

	control						GDNF+TGFβ1				
	1	2	3	4	5		1	2	3	4	5
Gata-2	1	1	1	1	1		1	1	1	1	1
Gata-3	1	1	0	0	0		1	1	0	0	1
Olf-1	0	1	1	0	1		0	1	1	0	1
Olf-1H	1	1	1	1	1		1	1	1	0	1
Pbx-1	1	1	1	1	0		1	1	1	1	0
LMO4	1	1	1	1	1		1	1	1	1	1
Id3	1	1	1	1	1		1	1	1	1	1
Dlx2	1	1	1	1	1		1	1	1	1	1
Sox2	1	1	1	1	0		1	1	1	1	1
Sox11	0	0	1	1	1		0	0	1	1	1
Bmp-2	1	1	1	1	1		1	1	1	1	1
Bmp-6	1	1	1	1	1		0	1	1	1	1
noggin	0	1	1	0	0		0	1	1	0	0
chordin	1	1	1	1	1		1	1	1	1	1
SMAD6	1	1	0	0	1		1	1	1	0	1
SMAD7	1	1	1	1	1		1	1	1	1	1
Msx1	1	1	1	0	0		1	1	1	0	0
Msx2	0	1	0	0	0		0	1	0	0	0
Hes-1	1	1	0	0	1		1	1	1	1	1
Hes-5	1	1	1	0	1		1	1	1	0	1
Hey1	1	1	1	1	1		1	1	1	1	1
Hey2	1	1	1	1	1		0	1	1	1	1
HeyL	1	1	1	1	1		1	0	1	1	1
MyT-1	1	1	1	1	1		0	1	1	1	1
MyT-2	0	1	1	0	1		0	1	1	0	1
MyT-3	1	1	1	1	1		1	1	1	1	1
SHH	1	1	0	0	0		0	1	0	0	0
Gli1	1	1	0	1	0		1	1	1	0	1
Gli2	1	0	1	0	1		0	0	0	0	0
Gli3	0	1	0	0	0		0	0	1	0	0
Zic1	0	0	0	1	0		0	0	0	1	0
Zic2	1	1	1	1	0		0	1	1	0	0
Zic3	0	0	1	0	0		0	1	1	0	0
Irx2a	1	1	0	1	1		0	1	1	1	1
Irx3	0	0	0	0	0		0	0	0	0	0
NN1	0	0	0	0	0		0	0	0	0	0
NN3	0	1	1	1	1		0	1	1	1	0
Ash-1	1	1	1	1	0		1	1	1	1	0
NeuroD1	1	1	0	1	1		1	1	0	1	1
NeuroD2	1	1	0	1	1		1	1	1	1	1
NeuroD3	0	0	0	0	1		0	0	0	0	1
NSCL1	1	1	1	1	1		1	1	1	1	1
NSCL2	0	0	0	0	1		0	0	0	0	1
Emx1	1	1	1	0	1		1	1	1	0	1
Emx2	0	0	0	0	1		0	0	0	0	1

	control						GDNF+TGFβ1				
	1	2	3	4	5		1	2	3	4	5
Gbx2	1	1	1	0	1		0	1	1	1	0
Otx1	1	1	1	1	1		1	1	1	1	1
Otx2	0	0	0	0	0		0	0	0	0	0
Pax6	1	0	0	1	1		1	0	0	1	1
Okt2	1	1	1	1	1		1	1	1	1	1
Brn2	1	0	1	0	0		0	0	1	1	0
Brn4	0	0	0	1	1		0	0	0	0	1
Brn5	1	1	1	1	1		1	1	1	1	1
Dlx7	1	1	0	1	1		1	1	1	1	1
Nkx2.5	1	1	0	0	0		1	1	0	0	0
Internexin	1	1	0	0	0		1	1	0	0	0
GFAP	0	0	0	0	0		0	0	0	0	0
A2B5	1	1	1	1	1		1	1	1	1	1
βIIItub	1	1	1	1	1		1	1	1	0	1
MAP2	0	0	0	0	1		0	0	1	0	1
NF 311	0	0	0	0	1		0	0	0	0	1
NF-P	1	1	1	1	1		1	1	1	1	1
RARb	1	1	1	1	1		0	1	1	1	1
RXRa	1	1	1	1	0		0	1	1	1	1
RXRb	0	1	1	1	1		0	1	1	1	1
desmin	1	1	1	1	0		1	1	1	1	1
SM-act	0	0	0	0	0		0	1	0	1	0
crhomogA	1	1	1	1	1		1	1	1	1	1
GRP	1	1	1	1	1		1	1	1	1	1
SR	1	1	1	1	1		1	1	1	1	1
NSE	1	1	1	1	1		1	1	1	1	1

N.B.: The numbers in the top row of the Table refer to different subjects; a value of "1" reflects mRNA expression; and a value of "0" connotes the absence of mRNA expression.

[0092] The effect of different external stimuli, such as various growth factors and cytokines and their combinations, on proliferation and differentiation in human NSCLCs was also examined in this example. For this purpose, cells in culture were treated with different biologically active factors that are known to stimulate differentiation or apoptosis. Suitable biologically active factors include a host of cytokines, such as TGF-β1, and different neurotrophic factors such as NGF, BDNF, NT-3, NT-4, alone or in combination. It will be appreciated, however, that any factor that affects cell survival and differentiation may be employed to evaluate the response of tumor subtypes to different treatment protocols. Correlation between the gene expression profile and response in proliferation/differentiation to treatments was identified (Table 16). The data established that certain external signals

(GDNF+TGFβ1) resulted in the activation of mixed developmental programs (neurons/ astrocytes/ oligodendrocytes/ smooth muscle cells) in different NSCLCs. O4, CNPase weak immunoreactivity was examined in the same cells that were MAP2+, A2B5, and desmin-positive. These data suggest that such activation of mixed differentiation programs finalizes in the execution of programmed cell death, and this type of a suicidal mechanism (through activation of "too many" developmental programs) as such presents an attractive target for cancer drug therapy.

<u>Table 16</u>

<u>Effect of TGFβ1, GDNF and BMP4 on the proliferation of lung tumor cells.</u>

	1	**2**	**3**	**4**	**5**
+TGFβ1	-	-	-	-	-
+GDNF	-	3.0±0.7↑	-	-	-
+GDNF + TGFβ1	6.0±1.0↓	-	-	-	3.9±0.9↑
+NT-4	-	-	-	-	-
+NT-4 + TGFβ1	-	2.6±0.3↑	-	-	-
+BMP-4	2.6±0.7↑	2.4±0.2↑	-	-	-
+BMP-4 + TGFβ1	-	-	-	-	-

[0093] Human NSCLC cells were grown for 6 days on laminin-coated 24-well plates in DMEM/F-12 media supplemented with B27 in the presence of TGFβ1 (100pg/ml), GDNF (100ng/ml) and BMP4 (100ng/ml). After 6 days cells were dissociated and cell number determined using hemocytometer. Values represent the relative change (in folds) in cell number normalized to the cell number of untreated cultures. Three independent experiments were performed to assess the changes in cell number. ↑ - enhanced proliferation compared to control; ↓ - reduced proliferation compared to control.

CONCLUSION

[0094] We have discovered that the various neoplastic molecular markers can be used to diagnose and direct the treatment of neoplastic diseases. The forgoing examples are not intended to limit the scope of the present invention, which is set forth in the following

claims. In particular, various equivalents and substitutions will be recognized by those of ordinary skill in the art in view of the foregoing disclosure, and these are contemplated to be within the scope of the invention.